

A. Harris  
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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/471,749

#6  
DATE: 03/31/2000  
TIME: 09:44:10

INPUT SET: S35194.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Hillman, Jennifer L.  
6 Corley, Neil C.  
7 Guegler, Karl J.  
8 Patterson, Chandra  
9 Baughn, Mariah  
10  
11 (ii) TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS  
12  
13 (iii) NUMBER OF SEQUENCES: 12  
14  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
17 (B) STREET: 3174 Porter Dr.  
18 (C) CITY: Palo Alto  
19 (D) STATE: CA  
20 (E) COUNTRY: USA  
21 (F) ZIP: 94304  
22  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Diskette  
25 (B) COMPUTER: IBM Compatible  
26 (C) OPERATING SYSTEM: DOS  
27 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
28  
29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER: 09/471,749  
31 (B) FILING DATE:  
32  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 09/078,402  
35 (B) FILING DATE:  
36  
37 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: Cerrone, Michael C.  
39 (B) REGISTRATION NUMBER: 39,132  
40 (C) REFERENCE/DOCKET NUMBER: PF-0519 US  
41  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: 650-855-0555  
44 (B) TELEFAX: 650-845-4166  
45  
46 (2) INFORMATION FOR SEQ ID NO:1:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/471,749

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48

(i) SEQUENCE CHARACTERISTICS:

49

(A) LENGTH: 480 amino acids

50

(B) TYPE: amino acid

51

(C) STRANDEDNESS: single

52

(D) TOPOLOGY: linear

53

54

(vii) IMMEDIATE SOURCE:

55

(A) LIBRARY: THP1PLB02

56

(B) CLONE: 157658

57

58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

59

60

61

Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp

62

1 5 10 15

63

Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val

64

20 25 30

65

Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly

66

35 40 45

67

Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg

68

50 55 60

69

Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu

70

65 70 75 80

71

Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu

72

85 90 95

73

Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu

74

100 105 110

75

Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu

76

115 120 125

77

Lys Ser Phe Leu Asp Leu Val Glu Leu Glu Lys Leu Asn Leu Val

78

130 135 140

79

Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His

80

145 150 155 160

81

Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln

82

165 170 175

83

Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys

84

180 185 190

85

Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser

86

195 200 205

87

Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val

88

210 215 220

89

Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro

90

225 230 235 240

91

Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile

92

245 250 255

93

Ile Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr

94

260 265 270

95

Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly

96

275 280 285

97

Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp

98

290 295 300

99

Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/471,749

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```

100      305      310      315      320
101 Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile
102      325      330      335
103 Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro
104      340      345      350
105 Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu
106      355      360      365
107 Asp Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu
108      370      375      380
109 Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp
110      385      390      395      400
111 Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser
112      405      410      415
113 His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg
114      420      425      430
115 Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly
116      435      440      445
117 Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr
118      450      455      460
119 Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr
120      465      470      475      480
121

```

## (2) INFORMATION FOR SEQ ID NO:2:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1PLB02
- (B) CLONE: 157658

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

136 GAAATTGCGC CACTGCACTC CAGCCTGGGC CACAGAGCGA GACTCTGTCT CAAAAAAGAA      60
137 GGAAAGAAAG AAAGAAAAAA AAAAACACTC GCAGTGTTTA CTCCTAACGC GTGGAACCTG      120
138 TGTCGACATC CACCCCGGT TACTGCATAC TCAGTCACAC AAGCCATAGC AGGAAACAGC      180
139 GAGCTTGCA GCTCACCGAC GAGTCTCAAC TAAAAGGGAC TCCCGGAGCT AGGGGTGGGG      240
140 ACTCGGCCTC ACACAGTGAG TGCCGGCTAT TGGACTTTTG TCCAGTGACA GCTGAGACAA      300
141 CAAGGACCAC GGGAGGAGGT GTAGGAGAGA AGCGCCGCGA ACAGCGATCG CCCAGCACCA      360
142 AGTCCGCTTC CAGGCTTTTCG GTTTCTTTGC CTCCATCTTG GGTGCGCCTT CCCGGCGTCT      420
143 AGGGGAGCGA AGGCTGAGGT GGCAGCGGCA GGAGAGTCCG GCCGCGACAG GACGAACTCC      480
144 CCCACTGGAA AGGATTCTGA AAGAAATGAA GTCAGCCCTC AGAAATGAAG TTGACTGCCT      540
145 GCTGGCTTTC TGTGACTGG CCCGGAGCTG TACTGCAAGA CCCTTGTGAG CTTCCCTAGT      600
146 CTAAGAGTAG GATGCTGCT GAAATCATCC ATCAGGTGTA AGAAGCACTT GATACAGATG      660
147 AGAAGGAGAT GCTGCTCTTT TGTGCCGGG ATGTTGCTAT AGATGTGGTT CCACCTAATG      720
148 TCAGGGACCT TCTGGATATT TTACGGGAAA GAGGTAAGCT GTCTGTCGGG GACTTGGCTG      780
149 AACTGCTCTA CAGAGTGAGG CGATTTGACC TGCTCAAACG TATCTTGAAG ATGGACAGAA      840
150 AAGCTGTGGA GACCCACCTG CTCAGGAACC CTCACCTTGT TTCGACTAT AGAGTGCTGA      900
151 TGGCAGAGAT TGGTGAGGAT TTGGATAAAT CTGATGTGTC CTCATTAATT TTCCTCATGA      960
152 AGGATTACAT GGGCCGAGGC AAGATAAGCA AGGAGAAGAG TTTCTTGGAC CTTGTGGTTG      1020

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/471,749

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```

153 AGTTGGAGAA ACTAAATCTG GTTGCCCCAG ATCAACTGGA TTTATTAGAA AAATGCCCTAA 1080
154 AGAACATCCA CAGAATAGAC CTGAAGACAA AAATCCAGAA GTACAAGCAG TCTGTTCAAG 1140
155 GAGCAGGGAC AAGTTACAGG AATGTTCTCC AAGCAGCAAT CCAAAAAGAGT CTCAAGGATC 1200
156 CTTCAAATAA CTTCAGGCTC CATAATGGGA GAAGTAAAGA ACAAAGACTT AAGGAACAGC 1260
157 TTGGCGCTCA ACAAGAACCA GTGAAGAAAT CCATTTCAGGA ATCAGAAGCT TTTTTCGCTC 1320
158 AGAGCATACC TGAAGAGAGA TACAAGATGA AGAGCAAGCC CCTAGGAATC TGCCGTGATAA 1380
159 TCGATTGCAT TGGCAATGAG ACAGAGCTTC TTCGAGACAC CTTCACTTCC CTGGGCTATG 1440
160 AAGTCCAGAA ATTCTTGCAAT CTCAGTATGC ATGGTATATC CCAGATTCTT GGCCAAATTTG 1500
161 CCTGTATGCC CGAGCACCGA GACTACGACA GCTTTGTGTG TGTCCCTGGTG AGCCGAGGAG 1560
162 GCTCCAGAG TGTGTATGGT GTGGATCAGA CTCACTCCGG GCTCCCCCTG CATCACATCA 1620
163 GGAGGATGTT CATGGGAGAT TCATGCCCTT ATCTAGCAGG GAAGCCAAAG ATGTTTTTTA 1680
164 TTCAGAACTA TGTGGTGTCA GAGGGCCAGG TGGAGGACAG CAGCCTCTTG GAGGTGGATG 1740
165 GGCCAGCGAT GAAGAATGTG GAATGCAAGG CTCAGAAGCG AGGGCTGTGC ACAGTTCACC 1800
166 GAGAAGCTGA CTTCTTCTGG AGCCTGTGTA CTGCGGACAT GTCCCTGCTG GAGCAGTCTC 1860
167 ACAGCTCACC ATCCCTGTAC CTGCAGTGCC TCTCCCAGAA ACTGAGACAA GAAAGAAAAC 1920
168 GCCCACTCCT GGATCTTCAC ATTGAACTCA ATGGCTACAT GTATGATTGG AACAGCAGAG 1980
169 TTTCTGCCAA GGAGAAATAT TATGTCTGGC TGCAGCACAC TCTGAGAAAAG AAAC TTATCC 2040
170 TCTCCTACAC ATAAGAAACC AAAAGGCTGG GCGTAGTGGC TCACACCTGT GATCCCAGCA 2100
171 CTTTGGGAGG CCAAGGAGGG CAGATCACTT CAGGTCAGGA GTTCGAGACC AGCCTGGCCA 2160
172 ACATGGTAAA CGCTGTCCCT AGTAAAAATA CAAAAATTAG CTGGGTGTGG GTGTGGGTAC 2220
173 CTGTATTCCC AGTTACTTGG GAGGCTGAGG TGGGAGGATC TTTTGAACCC AGGAGTTCAG 2280
174 GGTATAGCA TGCTGTGATT GTGCCTACGA ATAGCCACTG CATACCAACC TGGGCAATAT 2340
175 AGCAAGATCC CA 2352

```

## (2) INFORMATION FOR SEQ ID NO:3:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 642272

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

191 Met Glu Tyr Ala Met Lys Ser Leu Ser Leu Leu Tyr Pro Lys Ser Leu
192 1 5 10 15
193 Ser Arg His Val Ser Val Arg Thr Ser Val Val Thr Gln Gln Leu Leu
194 20 25 30
195 Ser Glu Pro Ser Pro Lys Ala Pro Arg Ala Arg Pro Cys Arg Val Ser
196 35 40 45
197 Thr Ala Asp Arg Ser Val Arg Lys Gly Ile Met Ala Tyr Ser Leu Glu
198 50 55 60
199 Asp Leu Leu Leu Lys Val Arg Asp Thr Leu Met Leu Ala Asp Lys Pro
200 65 70 75 80
201 Phe Phe Leu Val Leu Glu Glu Asp Gly Thr Thr Val Glu Thr Glu Glu
202 85 90 95
203 Tyr Phe Gln Ala Leu Ala Gly Asp Thr Val Phe Met Val Leu Gln Lys
204 100 105 110
205 Gly Gln Lys Trp Gln Pro Pro Ser Glu Gln Gly Thr Arg His Pro Leu

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```

206          115          120          125
207 Ser Leu Ser His Lys Pro Ala Lys Lys Ile Asp Val Ala Arg Val Thr
208          130          135          140
209 Phe Asp Leu Tyr Lys Leu Asn Pro Gln Asp Phe Ile Gly Cys Leu Asn
210          145          150          155          160
211 Val Lys Ala Thr Phe Tyr Asp Thr Tyr Ser Leu Ser Tyr Asp Leu His
212          165          170          175
213 Cys Cys Gly Ala Lys Arg Ile Met Lys Glu Ala Phe Arg Trp Ala Leu
214          180          185          190
215 Phe Ser Met Gln Ala Thr Gly His Val Leu Leu Gly Thr Ser Cys Tyr
216          195          200          205
217 Leu Gln Gln Leu Leu Asp Ala Thr Glu Glu Gly Gln Pro Pro Lys Gly
218          210          215          220
219 Lys Ala Ser Ser Leu Ile Pro Thr Cys Leu Lys Ile Leu Gln
220          225          230          235

```

## (2) INFORMATION FOR SEQ ID NO:4:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTNOT03
- (B) CLONE: 642272

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

236 AATGTTCTTT TGGCCACTGT GAAGCCTCAG GAAGGGGCTC GGATTGCTCA AGGACCCATG      60
237 GGAGAGAGGA GGCTTTGACT GGGCTGCCTG CCTGTGAGGT CTCTGGACTA GAGGTCCAAC      120
238 GCAGTCCAGC TGACAAGGAT GGAATACGCC ATGAAGTCCC TTAGCCTTCT CTACCCCAAG      180
239 TCCCTCTCCA GGCATGTGTC AGTGCGTACC TCTGTGGTGA CCCAGCAGCT GCTGTCCGAG      240
240 CCCAGCCCCA AGGCCCCCAG GGCCCGGCCG TGCCGCGTAA GCACGGCGGA TCGAAGCGTG      300
241 AGGAAGGGCA TCATGGCTTA CAGTCTTGAG GACCTCCTCC TCAAGGTCCG GGACACTCTG      360
242 ATGCTGGCAG ACAAGCCCTT CTTCCCTGGT CTGGAGGAAG ATGGCACAAC TGTAGAGACA      420
243 GAAGAGTACT TCCAAGCCCT GGCAGGGGAT ACAGTGTTCa TGGTCCCTCCA GAAGGGGCAG      480
244 AAATGGCAGC CCCCATCAGA ACAGGGGACA AGGCACCCAC TGTCCCTCTC CCATAAGCCT      540
245 GCCAAGAAGA TTGATGTGGC CCGTGTAACG TTTGATCTGT ACAAGCTGAA CCCACAGGAC      600
246 TTCATTGGCT GCCTGAACGT GAAGGCGACT TTTTATGATA CATACTCCCT TTCCTATGAT      660
247 CTGCACTGCT GTGGGGCCAA GCGCATCATG AAGGAAGCTT TCCGCTGGGC CTTCTTCAGC      720
248 ATGCAGGCCA CAGGCCACGT ACTGCTTGGC ACCTCCTGTT ACCTGCAGCA GCTCCTCGAT      780
249 GCTACGGAGG AAGGGCAGCC CCCCAGGGG AAGGCCTCAT CCCTTATCCC GACCTGTCTG      840
250 AAGATACTGC AGTGAAAGCC CAAGTCCTTG GAAGCTTTCC CCAGTGAAGG ACTGACTGGG      900
251 GGCCTCACGC TTAACCTGGT GTGCCCACAA GCCTGGCAGC TGTAAGAGCCG CGAACCTCCC      960
252 CACACCTCCC TCACCGCGCA GGACCTGAG TGAGGAGGAG GAGCTGGAAA CCTGGGGTGG      1020
253 GTTGGCCAAA GGAGAACCTC AAGCTCCTGG CCTGATCCAG CTCCTTCCTG CCCAAGGCAG      1080
254 CTTAGCCCAT CCAGACTGGT CCTGAAGTCT GTCCCTCCAT TGGCATGAAG TCTGCCCCCTT      1140
255 AGCAATCCGG CCTCGCAGGC TGTACTTTCA TGGTGTCTC TACCTTCTGG CCCCATCCC      1200
256 GGAACATTCC TGAGTGAATT CGCAAGCGCA CTAGCATGTG ATATTAGGA GTTGTCAATA      1260
257 AATTATTGAG GCTGAAAAAA AAAA
258

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/471,749**

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Line

Error

Original Text